RAW SEQUENCE LISTING
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Application Serial Number: 09/955,737

Source: /FwJ/6

Date Processed by STIC: 8/6/04

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Revised 05/17/04

RAW SEQUENCE LISTING   DATE: 08/06/2004
PATENT APPLICATION: US/09/955,737   TIME: 10:54:14

    Input Set : A:\16163-015001.TXT
    Output Set: N:\CRF4\08062004\I955737.raw

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 4 <110> APPLICANT: Chopra , Rajiv
 5         Svenson, Kristine
 6         Annis, Bethany
 7         Akopian, Tatos N.
 8         Bard, Jonathan A.
 9         Stahl, Mark L.
10         Somers, William Stuart
13 <120> TITLE OF INVENTION: CRYSTAL STRUCTURE OF BACE AND USES
14         THEREOF
16 <130> FILE REFERENCE: 16163-015001
18 <140> CURRENT APPLICATION NUMBER: US 09/955,737
19 <141> CURRENT FILING DATE: 2001-09-19
21 <150> PRIOR APPLICATION NUMBER: US 60/234,576
22 <151> PRIOR FILING DATE: 2000-09-22
24 <160> NUMBER OF SEQ ID NOS: 6
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 501
30 <212> TYPE: PRT
31 <213> ORGANISM: Homo sapiens
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37             20                  25                  30
38 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
39             35                  40                  45
40 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
41      50                  55                  60
42 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
43 65                  70                  75                  80
44 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
45             85                  90                  95
46 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
47             100                 105                 110
48 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
49         115                 120                 125
50 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
51      130                 135                 140
52 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
53 145                 150                 155                 160
54 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
55             165                 170                 175
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57             180                 185                 190
58 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
59         195                 200                 205
60 Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
61     210                 215                 220
62 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
63 225                 230                 235                 240
64 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
65                 245                 250                 255
66 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
67             260                 265                 270
68 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
69     275                 280                 285
70 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
71     290                 295                 300
72 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
73 305                 310                 315                 320
74 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
75             325                 330                 335
76 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
77             340                 345                 350
78 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
79         355                 360                 365
80 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
81     370                 375                 380
82 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
83 385                 390                 395                 400
84 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
85             405                 410                 415
86 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
87             420                 425                 430
88 Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
89         435                 440                 445
90 Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
91     450                 455                 460
92 Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
93 465                 470                 475                 480
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97             500
99 <210> SEQ ID NO: 2
100 <211> LENGTH: 695
101 <212> TYPE: PRT
102 <213> ORGANISM: Homo sapiens
104 <400> SEQUENCE: 2
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106   1             5                 10                  15
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107 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
108             20              25              30
109 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
110         35              40              45
111 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
112     50              55              60
113 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
114 65              70              75              80
115 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
116             85              90              95
117 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
118         100             105             110
119 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
120         115             120             125
121 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
122     130             135             140
123 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
124 145             150             155             160
125 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
126             165             170             175
127 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
128         180             185             190
129 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
130         195             200             205
131 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
132     210             215             220
133 Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
134 225             230             235             240
135 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
136             245             250             255
137 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
138             260             265             270
139 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
140     275             280             285
141 Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
142     290             295             300
143 Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
144 305             310             315             320
145 Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
146             325             330             335
147 Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
148         340             345             350
149 Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
150         355             360             365
151 Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
152     370             375             380
153 Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
154 385             390             395             400
155 Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
```

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156                 405              410              415
157 Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
158         420              425              430
159 Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
160         435              440              445
161 Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
162     450              455              460
163 Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
164 465             470              475              480
165 Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
166             485              490·             495
167 Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
168         500              505              510
169 Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
170         515              520              525
171 Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
172     530              535              540
173 Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
174 545             550              555              560
175 Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
176             565              570              575
177 Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
178         580              585              590
179 Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
180         595              600              605
181 His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
182     610              615              620
183 Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
184 625             630              635              640
185 Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
186             645              650              655
187 His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
188             660              665              670
189 His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
190         675              680              685
191 Phe Phe Glu Gln Met Gln Asn
192     690              695
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195 <211> LENGTH: 9
196 <212> TYPE: PRT
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: APP inhibitor peptide
202 <221> NAME/KEY: VARIANT
203 <222> LOCATION: 5
204 <223> OTHER INFORMATION: Xaa = Sta = Statine
206 <400> 3
207 Ser Glu Val Asn Xaa Val Ala Glu Phe
208 1               5
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212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Primer
218 <400> SEQUENCE: 4
219 gctctagaac ccagcacggc atccggctg                                      29
221 <210> SEQ ID NO: 5
222 <211> LENGTH: 42
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Primer
229 <400> SEQUENCE: 5
230 ccaagcatgc ggccgcaata ggctatggtc atgagggttg ac                       42
232 <210> SEQ ID NO: 6
233 <211> LENGTH: 12
234 <212> TYPE: PRT
235 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <223> OTHER INFORMATION: Synthetically generated peptide
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     241 <222> LOCATION: 1
     242 <223> OTHER INFORMATION: Xaa = Abz = amino benzoic acid
W--> 244 <221> VARIANT
     245 <222> LOCATION: 12
     246 <223> OTHER INFORMATION: Xaa = = Dpa = 9,10-diphenylanthracene
W--> 248 <400> 6
W--> 249 Xaa Ser Glu Val Asn Leu Asp Ala Glu Phe Arg Xaa
     250  1                     5                 10
```

FYI: Xaa can only represent a single amino acid nothing else

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/06/2004
PATENT APPLICATION: **US/09/955,737**   TIME: 10:54:15

Input Set : **A:\16163-015001.TXT**
Output Set: **N:\CRF4\08062004\I955737.raw**

<u>Please Note:</u>
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.**

Seq#:3; Xaa Pos. 5
Seq#:6; Xaa Pos. 1,12

VERIFICATION SUMMARY   DATE: 08/06/2004
PATENT APPLICATION: **US/09/955,737**   TIME: 10:54:15

Input Set : **A:\16163-015001.TXT**
Output Set: **N:\CRF4\08062004\I955737.raw**

L:202 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:206 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:240 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:244 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:248 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0